IN THE TITLE

Please replace the title with the following amended title:

~~NEW~~ CHEMOKINE PANEC-2 POLYNUCLEOTIDES, POLYPEPTIDES, ANTIBODIES AND METHODS OF MAKING AND USING THEM ~~EXPRESSED IN PANCREAS~~

IN THE SPECIFICATION

Please replace the two paragraphs on page 5, line 18-24, with the following amended paragraphs:

~~Figure 2 displays~~ Figures 2A and 2B display the nucleotide sequence for panec-2 and the predicted amino acid (aa) sequence of the pancreas expressed chemokine, PANEC-2.

~~Figure 3 shows~~ Figures 3A, 3B and 3C show the aa alignment of PANEC-1 and PANEC-2 with other human chemokines of the C-C family. Alignments shown were produced using the multisequence alignment program of DNASTAR software (DNASTAR Inc, Madison WI) (Majority = SEQ ID NO:5; MIP 1α = SEQ ID NO:6; MIP 1β = SEQ ID NO:7; RANTES = SEQ ID NO:8; MCP-1 = SEQ ID NO:9; MCP-2 = SEQ ID NO:10; MCP-3 = SEQ ID NO:11).

Please replace the paragraph beginning on page 5, line 29 and ending on page 6, line 1, with the following amended paragraph:

Figure ~~5~~ 6 shows a relatedness tree of human C-C chemokines. The phylogenetic tree was generated by phylogenetic tree program of DNASTAR software using the Clustal method with the PAM250 residue weight table.

IN THE CLAIMS

Summary:

Claims 19, 21-22 and 24-59 are canceled, without prejudice or disclaimer.

Claims 1, 2, 5, 10, 12 and 18 are amended.

New claims 60-61 are presented.

Listing of Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Currently Amended.) An isolated polypeptide selected from the group consisting of:

a) a polypeptide comprising an amino acid sequence ~~selected from the group consisting~~ of ~~SEQ ID NO:2 and~~ SEQ ID NO:4,

b) a polypeptide encoding an allelic or recombinant variant of the ~~comprising a naturally occurring amino acid sequence at least 90% identical to an~~ amino acid sequence ~~selected from the group consisting~~ of ~~SEQ ID NO:2 and~~ SEQ ID NO:4, wherein said variant

iii) has an insertion or deletion of 1-5 amino acids as compared with SEQ ID NO:4; and/or

ii) has one or more amino acid substitutions as compared with SEQ ID NO:4, and has the amino acid sequence of SEQ ID NO:4 at amino acids 1, 4, 6, 7 10, 15, 19, 31-32, 35, 38, 41, 48, 52, 54, 57-58, 60-61, 64, 71, 75-78, 80, 82-84 and 90,

iii) and further wherein the variant has chemokine activity,

c) a biologically active fragment of a polypeptide having an amino acid sequence ~~selected from the group consisting~~ of ~~SEQ ID NO:2 and~~ SEQ ID NO:4, wherein said fragment has chemokine activity, and

d) an ~~immunogenic~~ immunogenically active fragment of a polypeptide having an amino acid sequence ~~selected from the group consisting~~ of ~~SEQ ID NO:2 and~~ SEQ ID NO:4,

wherein said immunogencially active fragment is capable of generating an antibody that specifically binds to the polypeptide of SEQ ID NO:4.

2. (Currently Amended.) An isolated polypeptide of claim 1, having ~~a~~ the sequence ~~selected from the group consisting~~ of ~~SEQ ID NO:2 and~~ SEQ ID NO:4.

3. (Original.) An isolated polynucleotide encoding a polypeptide of claim 1.

4. (Original.) An isolated polynucleotide encoding a polypeptide of claim 2.

5. (Currently Amended.) An isolated polynucleotide of claim 4, having ~~a~~ the sequence ~~selected from the group consisting~~ of ~~SEQ ID NO:1 and~~ SEQ ID NO:3.

6. (Original.) A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.

7. (Original.) A cell transformed with a recombinant polynucleotide of claim 6.

8. (Original.) A transgenic organism comprising a recombinant polynucleotide of claim 6.

9. (Original.) A method for producing a polypeptide of claim 1, the method comprising:

a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide encoding the polypeptide of claim 1, and

b) recovering the polypeptide so expressed.

10. (Currently Amended.) A method of claim 9, wherein the polypeptide comprises ~~an~~ the amino acid sequence ~~selected from the group consisting~~ of ~~SEQ ID NO:2 and~~ SEQ ID NO:4.

11. (Original.) An isolated antibody which specifically binds to a polypeptide of claim 1.

12. (Currently Amended.) An isolated polynucleotide comprising a sequence selected from the group consisting of:

a) a polynucleotide comprising a polynucleotide sequence ~~selected from the group consisting~~ of ~~SEQ ID NO:1 and~~ SEQ ID NO:3,

b) a naturally occurring polynucleotide ~~comprising a polynucleotide~~ sequence variant ~~at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1 and~~ of SEQ ID NO:3, wherein said variant encodes an amino acid sequence of SEQ ID NO:4, and wherein said variant

i) differs by an insertion or deletion of 1-5 amino acids as compared with SEQ ID NO:4; and/or

ii) has one or more amino acid substitutions as compared with SEQ ID NO:4, and has the amino acid sequence of SEQ ID NO:4 at amino acids 1, 4, 6, 7 10, 15, 19, 31-32, 35, 38, 41, 48, 52, 54, 57-58, 60-61, 64, 71, 75-78, 80, 82-84 and 90,

iii) and further wherein the variant has chemokine activity,

ii a polynucleotide having a sequence fully complementary along its length to a polynucleotide of a),

ii a polynucleotide having a sequence fully complementary along its length to a polynucleotide of b) and

ii an RNA equivalent of a)-d).

13. (Original.) An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 12.

14. (Original.) A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 12, the method comprising:

a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and

b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

15. (Original.) A method of claim 14, wherein the probe comprises at least 60 contiguous nucleotides.

16. (Original.) A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 12, the method comprising:

a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and

b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

17. (Original.) A composition comprising a polypeptide of claim 1 and a pharmaceutically acceptable excipient.

18. (Currently Amended.) A composition of claim 17, wherein the polypeptide has ~~an~~ the amino acid sequence ~~selected from the group consisting~~ of ~~SEQ ID NO:2 and~~ SEQ ID NO:4.

Claim 19. (Canceled.)

20. (Original.) A method for screening a compound for effectiveness as an agonist of a polypeptide of claim 1, the method comprising:

a) exposing a sample comprising a polypeptide of claim 1 to a compound, and

b) detecting agonist activity in the sample.

Claims 21 - 22. (Canceled.)

23. (Original.) A method for screening a compound for effectiveness as an antagonist of a polypeptide of claim 1, the method comprising:

a) exposing a sample comprising a polypeptide of claim 1 to a compound, and

b) detecting antagonist activity in the sample.

Claims 24 - 59. (Canceled.)

60. (New.) An isolated polynucleotide of claim 12, wherein said polynucleotide is non-genomic.

61. (New.) An isolated polynucleotide of claim 12, wherein said polynucleotide encodes, without introns, the polypeptide.

IN THE DRAWINGS

Amendments to the Drawings:

The attached sheets of drawings includes changes to Figs. 1-3.

New Fig. 1 replaces the original Fig. 1, with margins and type size corrected.

New Fig. 2A and 2B replace the original Fig. 2, with margins and type size corrected.

New Fig. 3A, 3B and 3C replace the original Fig. 3, with margins and type size corrected.

Attachment: Replacement Sheets Fig. 1, Figs. 2A and 2B, and Figs. 3A, 3B and 3C.

REMARKS

Copending application

Applicants direct the Examiner's attention to the fact that there is a copending case, i.e., the parent application of the instant case, which is being and has been examined by Examiner Marschel for the past several years. In that case, Applicants already received a complete examination of the claims to polynucleotides, etc., encoding SEQ ID NO:4 (as well as polynucleotides, etc., encoding SEQ ID NO:2). Applicants have recently filed an Amendment in the copending case limiting it to the inventions related to SEQ ID NO:2.

Restriction Requirement

In response to the Restriction Requirement, Applicants to elect the claims of one of Group III or Group IV, directed, *inter alia*, to nucleic acids, vectors and host cells. It is assumed that Group III and Group IV were supposed to be different, based on whether the claims were directed to SEQ ID NO:1 (or nucleic acids encoding a polypeptide of SEQ ID NO:2), or to SEQ ID NO:3 (or nucleic acids encoding a polypeptide of SEQ ID NO:4). Applicants elect, with traverse, to have examined the claims directed to nucleic acids, vectors and host cells comprising nucleic acids of SEQ ID NO:3 (or nucleic acids encoding a polypeptide of SEQ ID NO:4).

Applicants traverse this election on a number of grounds. First, it is noted that a complete examination of this Group (including BOTH SEQ ID NO:1, nucleic acids encoding a polypeptide of SEQ ID NO:2, SEQ ID NO:3, and nucleic acids encoding a polypeptide of SEQ ID NO:4) were examined in the parent application, and the only remaining objections to the claims relating to polynucleotides of SEQ ID NO:3 and nucleic acids encoding a polypeptide of SEQ ID NO:4 were objections to the scope of the claims (addressed below) and the possible interference with the claims of newly issued patent 6,518,046 to Li et al. Moreover, in the parent application, Applicants submitted a very thorough search for all of the inventions claimed in that application, including the polypeptides encoded by the claimed and elected polynucleotides and antibodies relating to both chemokines, and for the methods of making and using them, and provided sequence alignments to facilitate the Examiner's consideration of those references.

Therefore, Applicants submit that there would be no undue burden for the Examiner of the instant application to fully examine ALL of Applicants claims relating to polynucleotides of SEQ ID NO:3 and nucleic acids encoding a polypeptide of SEQ ID NO:4 (presumably the invention of Group IV), as well as the claims of Group II, VI, VIII, X and XII. Particularly in view of the many delays that have occurred in the prosecution of this patent application (the parent application has been and still is pending after almost 8-1/2 years), including a three year suspension, Applicants submit that it would be the most equitable treatment of the instantly claimed invention to have the entirety of their invention relating to polynucleotides of SEQ ID NO:3 and nucleic acids encoding a polypeptide of SEQ ID NO:4 to be examined together in the instant application. Reconsideration and reformulation of the restriction requirement in accordance with this request is therefore earnestly solicited.

In any case, Applicants reserve the right to prosecute non-elected subject matter in subsequent divisional applications.

Comments regarding support for amendments to the drawings and specification:

The drawings are corrected by submission of the attached replacement pages. The corrections are all formal in nature, putting the Figures in compliance with margin and font size requirements, and do not contain any substantive amendments. Amendments to the specification have been made to reflect the new Figure numbering.

Comments regarding support for amendments to the claims:

Amendments to the language "immunogenically active" instead of "immunogenic" are primarily grammatical in nature.

Support for the language "allelic or recombinant variant" added to the claims, e.g., claims 1 and 12, can be found on page 8, lines 1-2: "The DNAs which encode PANEC-1 and PANEC-2 may also include allelic or recombinant variants and mutants thereof."

Support for the various limitations in the amounts and types of insertions, deletions and substitutions are mathematical calculations or sequence selections based upon the teaching of the specification, including Fig. 3 (now 3A, 3B and 3C), which compares PANEC-2 to its three closest prior art molecules known at the time of the invention, namely MIP-1a, MIP-1b and RANTES. For

example, in the amendments to claims 1 and 12, the language "has an insertion or deletion of 1-5 amino acids as compared with SEQ ID NO:2" is supported on page 7, lines 6-7.

Similarly, in the amendments to claim 12, the language has one or more amino acid substitutions as compared with SEQ ID NO:4, and has the amino acid sequence of SEQ ID NO:4 at amino acids 1, 4, 6, 7 10, 15, 19, 31-32, 35, 38, 41, 48, 52, 54, 57-58, 60-61, 64, 71, 75-78, 80, 82-84 and 90" is supported by the language in the paragraph bridging pages 6-7: "may be found by comparing the sequence of the particular PANEC with that of homologous cytokines and minimizing the number of aa sequence changes made in regions of high homology"; by counting the number of amino acid changes between PANEC-2 with respect to all three of the prior art MCPs disclosed in the specification. Again, the disclosure in the specification in the paragraph bridging pages 6-7, ("may be found by comparing the sequence of the particular PANEC with that of homologous cytokines and minimizing the number of aa sequence changes made in regions of high homology") provides guidance for and supports identification of specific amino acid residues of PANEC-2 which should be retained in a variant, i.e., wherein 2 of the 3 MIPs and/or RANTES ("homologous cytokines") have the same amino acid at a specific location ("minimizing the number of aa sequence changes made in regions of high homology") as PANEC-2, and by only allowing sequence variation at residues where PANEC-2 differs from at least 2 of the 3 MIPs and/or RANTES. Those specific sequences where changes should not be made are easily identified with reference to Fig. 3. It is clear that there can be substitutions at the other amino acid positions which can be made without reading on the prior art chemokines. While support for the list of specific amino acid sequences of PANEC-2 which are preferably invariant is not literally present, it can be fairly construed by reference to Fig. 3.

Title Amendment

The title of the application has been amended to be more clearly descriptive of the claimed chemokine polynucleotides, polypeptides and antibodies thereto, and methods of making and using them, corresponding to the amendment made in the parent application.

Regarding possible issues under 35 U.S.C. § 112, first paragraph, raised in the parent application

In the Office Action mailed March 3, 2003, in the parent application, on page 8, paragraph bridging to page 9, Examiner Marschel states that the rejected claims "are directed to encompass full gene sequences, sequences that hybridize to SEQ ID NOs: 1 or 3."

First, claims to SEQ ID NO:1 are no longer pending in this application, although the following arguments apply equally to the claims to PANEC-1 that have been canceled herein.

Second, the rejected claims do not recite the words "full gene" in describing the claimed polynucleotide sequences, nor do they claim sequence that "hybridize to SEQ ID NO:3." The claim is directed to "*[a]n isolated polynucleotide* comprising a polynucleotide sequence selected from the group consisting of: ... *a polynucleotide sequence encoding an amino acid sequence of SEQ ID NO:4* ...". The plain meaning of the words in the claim, particularly as taken in view of the state of the art (including literally thousands of other gene patents issued by the USPTO that use essentially identical language to the instant claim 1), the disclosure in the specification and the prosecution history of the parent application over 8.5 years of pendancy of this case make it clear that the claimed sequences do not encompass genomic DNA, nor an isolated chromosome on a microscope slide (as was discussed at the interview with Examiner Marschel on June 26, 2003), said hypothetically encompassed sequences clearly failing to be either useful under 35 U.S.C. § 101 or novel under § 102. Applicants note that in the patent references cited by Examiner Marschel as encompassing genomic sequences, such was accomplished by the patentees' express intent to include genomic sequences, which intent is not present herein, either in the specification or file history.

The Examiner (and the courts) are directed by *Genentech Inc v. The Wellcome Foundation Ltd.*, 31 USPQ2d 1161(Fed. Cir. 1994) to construe claims in such a way as to preserve validity, particularly when there is only one reasonable way of construing the claims asserted by Applicants during prosecution. As the Federal Circuit said:

> An appropriate method for resolving the issue [the proper scope of the phrase "human tissue plasminogen activator" appearing in the claims] is to avoid those definitions upon which the PTO could not reasonably have relied when it issued the patent. That is an appropriate method to follow because it avoids the possibility of an applicant obtaining in court a scope of protection which encompasses subject matter that, through the conscious efforts of the

> applicant, the PTO did not examine. An applicant should not be able deliberately to narrow the scope of examination to avoid during prosecution scrutiny by the PTO of subject matter with the objective of more quickly obtaining a patent (or avoiding the risk of an estoppel), and then obtain in court, either literally or under the doctrine of equivalents, a scope of protection which encompasses that subject matter. See *North American Vaccine Inc.*, 7 F.3d at 1577, 28 USPQ2d at 1337. [footnote omitted]

Applicants expressly assert that Examiner Marschel's concern that the scope of Applicants' claims might be extended, by torturous claim construction, to include genomic and/or chromosomal sequences not supported in the specification is therefore misplaced, as Applicants have clearly not only disclaimed it by the plain meaning of the claims, but also expressly herein as well as in previous prosecution papers in the parent application. No court or member of the public could reasonably read them so broadly.

In any case, Applicants have proposed alternative claim language, supported by the specification and the knowledge of those of skill in the art, in claim 60 ("non-genomic," supported as the negative of the definition in the specification on page 10, lines 2-3, of genomic sequences as "including promoters, enhancer elements and introns of the respective naturally occurring panecs"), and in claim 61 ("encodes, without introns," supported in the same place in the specification).

Further Comments on Enablement of Protein/Antibody Claims and Methods of Use

Upon determination of allowability of the polynucleotide claims, Applicants have requested rejoinder of all of the pending claims related to the core invention of PANEC-2, including polypeptides, antibodies that specifically bind to the polypeptides and methods of use of all of the compositions of matter. In particular in view of the complete examination of the claims of the polynucleotids encoding the polypeptide of SEQ ID NO:4 in the parent application, and the IDS submitted herewith, Applicants reiterate that there should be no undue burden on the Examiner to examine the full scope of Applicants' invention. This is even more particularly in view of the already 8.5 year pendency of the instant claims, including pendency during the prolonged prosecution in the parent application.

Comments regarding the prior art cited in the parent application

The Examiner's attention is directed to the attached PTO Form 1449, which identifies references that can be found in the parent application file with the Information Disclosure Statement

filed October 7, 2002, that is named "PANEC-2" at the top of the page. In particular, the Examiner's attention is directed to U.S. Serial Number 08/294,251, filed August 23, 1994 (PANEC-2 IDS Reference I), which is the priority document for PCT application WO 9606169 (Reference II), filed June 5, 1995. A continuation-in-part application of 08/294,251 was apparently filed in the PCT on June 6, 1995, and its corresponding National Phase (35 U.S.C. § 371) counterpart (USSN 08/793,381) was issued earlier this year as US 6,518,046 (made of record by the Examiner in the Office Action dated March 3, 2003). Applicants believe that this corresponding '381 application may have been the basis upon which the parent of the instant application was previously suspended for over two years after it was allowed, because it might eventually have allowable conflicting claims. Applicants wish to bring to the Examiner's attention the following facts and information regarding the priority document for this issued patent, as well as other documents mentioned in the attached PTO Form 1449 which can be found in the parent application file:

- The priority application U.S. Serial Number 08/294,251 (hereafter "the '251 application"), assigned to Human Genome Sciences, Inc., was obtained by Applicants from the Australian Patent Office, with which it is presumed to have been filed during the Australian National Stage filing of PCT application WO 9606169.
- The '251 application as received from the Australian Patent Office included **TWO** Sequence Listings, one apparently filed with the '251 application on its initial filing date, containing 2 sequences ("the first Sequence Listing"; marked in Ref. I as " '251 SEQ ID NO:1 and 2") and a second Sequence Listing apparently filed at a later date, which contained 6 sequences ("the second Sequence Listing"; marked in Ref. I as " '251 2nd SEQ ID NO:1 and 2").
- In addition, there were two drawing figures provided with the application as received from the Australian Patent Office. See the pink tabs on Ref. I filed in the parent application with the IDS filed on October 7, 2002 in the parent application.
- The first Sequence Listing is numbered as pages 31-33 of the specification. On page 32 of the specification, SEQ ID NO:1 is disclosed as having 378 nucleotides; this is a **VERY** different polynucleotide sequence from that of PANEC-2 (SEQ ID NO:3) of the instant application. On page 33, the corresponding protein SEQ ID NO:2 is disclosed as having 125 amino acids; this is a **VERY** different amino acid sequence from that of PANEC-2 (SEQ ID NO:4) of the

instant application. See the sequence comparisons attached to Ref. I at the end of the document.

- On page 3 of the '251 specification, Figure 1 is described as displaying "the cDNA and corresponding deduced amino acid sequence of Ckβ-9" and that "[t]he initial 22 [sic: 23 from the originally filed, first Sequence Listing] amino acids represent the leader sequence such that the putative mature polypeptide comprises 102 amino acids." However, the Figure 1 attached to the document sent by the Australian Patent Office clearly does not reflect sequences of that length; instead, the sequences in this Figure 1 (presumably filed with or after the second Sequence Listing, as they are found after the second Sequence Listing at the end of the specification of '251 and after the Abstract) have, respectively 405 nucleotides and 134 amino acids. Again, see the sequence comparisons attached to Ref. I.
- The second Sequence Listing submitted in the '251 application (no page numbers) has for SEQ ID NO:1 a **405** nucleotide sequence. This sequence differs from the first filed SEQ ID NO:1 in that there is a deletion of a "T" nucletotide at nucleotide 284, and the sequence continues for an additional 29 nucleotides past the end of the SEQ ID NO:1 listed in the first Sequence Listing.
- The second Sequence Listing submitted in the '251 application (no page numbers) has for SEQ ID NO:2 a **134** amino acid sequence. This sequence differs from the first filed SEQ ID NO:2 in that there is a different amino acid at amino acid 95 (corresponding to amino acid 72 of the "mature" protein, according to the numbering in the Sequence Listing), a completely different sequence from amino acid 95 -125 (corresponding to amino acids 72-102 of the "mature protein, according to the numbering in the Sequence Listing), and the amino acid sequence continues for an additional 9 amino acids past the end of the SEQ ID NO:1 listed in the first Sequence Listing for a total of 134 amino acids.

Applicants respectfully submit that it is *prima facie* apparent that the first Sequence Listing filed in the '251 application did not disclose or support the polynucleotide or amino acid sequences disclosed in either the subsequently filed second Sequence Listing or subsequently filed Figure 1 (see the sequence comparisons attached to Ref. I). It is submitted to be clear from the specification that the '251 application **as filed** was directed to a shorter and incorrect polynucleotide and amino acid sequence, which the Applicants of the '251 application attempted to correct by submitting a second

Sequence Listing and Figure 1 which do not correspond to the sequences described in the specification.

The instant Applicants respectfully submit that the second Sequence Listing and apparent replacement Fig. 1 were and are new matter to the '251 application as filed, and are entitled only to the PCT priority date in the 6,518,046 patent that issued. If those replacement papers were allowed to be submitted in the '251 application, Applicants submit that they should not be given any consideration, and that any alleged priority claimed by the Applicants of the '251 application in this or any later-filed application as of the August 1994 filing date, including any CIP application correcting the sequences in accordance with the second Sequence Listing or the apparently later filed Figure 1, should be disallowed. To the instant Applicants' knowledge, the earliest priority date to which HGS is entitled for the full 134 amino acid sequence (and full 402 nucleotides encoding it [HGS counted the stop codon at the end to arrive at 405 nucleotides]) corresponding to the instant Applicants' 134 amino acid sequence and 402 nucleotides encoding it, is June 5, 1995, which was the filing date of the PCT application WO 9606169 which designated the US, assuming that a corresponding US National Phase application or other US application claiming priority to it, is now pending before the USPTO.

Since a priority claim to the longer sequences as represented in the later filed second Sequence Listing and Figure 1 cannot properly be made based on the '251 application as filed, and the instant Applicants respectfully submit that the effective filing date of the instant application is more than three months prior to the effective filing date of the PCT application WO 9606169 (assuming it designated the US and assuming that a corresponding US National Phase application or proper continuation application claiming priority to that US National Phase application is now pending before the USPTO), Applicants further submit that, upon allowance of the claims of the instant application, the instant application should immediately issue as a US patent, as no suspension based upon the priority of the sequences **as filed** in the HGS '251 application would be proper.

At the very least, since the instant Applicants' allowable claims would be *prima facie* entitled to an effective filing date over 3 months prior to the effective filing date of any claims of HGS to the same or similar sequence, the instant Applicants submit that they should be entitled to be deemed the Senior Party, and their application should be allowed to issue, with the burden being shifted to HGS to make the necessary statements and affidavit under 37 C.F.R. § 1.608(b). See, e.g., M.P.E.P § 2303:

"Interferences will not be declared between pending applications if there is a difference of more than 3 months in the effective filing dates of the oldest and the next oldest applications of a simple character ...". Applicants submit that the "simple character" requirement is met by the ease of comparing the sequences and the effective filing dates of each application. Therefore, there is no reason to delay issuance of the present claims directed to PANEC-2 based on the HGS 6,518,046 patent.

Nevertheless, assuming the patentees are entitled to their earliest priority date for at least a portion of the claims directed to their deposited "human cDNA contained in ATCC Deposit No. 75803," Applicants submit that there remains a question regarding whether the sequences contained in that deposited cDNA indeed encodes a polypeptide of Applicants' SEQ ID NO:4, or has the same sequence as SEQ ID NO:3.

In addition to the '251 application and the continuation-in-part application that ultimately issued as the 6,518,046 patent, Applicants direct the Examiner's attention to the following patent publications (none of which appear to have resulted in issuance of a US patent) and other publications. Nevertheless, in the interest of completing the record, this information also included in the IDS for PANEC-2.

- **Reference III -- WO 96/25497** (assignee Incyte): This is the instant assignee Incyte's PCT application, which claims priority to the parent of the instant application.
- **Reference IV -- WO 98/14581** (assignee Schering Corporation): The claimed US priority applications were filed in 1996 and 1997, over **a year** after the instant application was filed. The nucleotide sequence is almost identical and the protein sequence is 100% identical to the instantly claimed PANEC-2 sequences.
- **Reference V -- WO 00/14581** (assignee Chiron Corporation): The claimed US priority application was filed December 31,1998, almost **4 years** after the instant application was filed. The nucleotide sequence and the protein sequence are 100% identical to the instantly claimed PANEC-2 sequences.
- **References VI-VIII**: These are all printed publications, including GenBank submissions, that became available to the public over a year after the instant application was filed. For the record, these references (to Hedrick et al., including the inventors of Ref. IV) relate to the same chemokine as claimed in Ref. IV (see the sequence comparisons at the tabs at the end of Refs. VI-VIII).

Applicants therefore submit that they are entitled to a prompt notice of Allowability of the instant application, and courteously solicit the Examiner's consideration Applicants' request for continuation of examination of the instant application to the non-elected claims relating to PANEC-2, so that the application might issue in the most expeditious manner possible, and thereby the claims would lose less of the remaining foreshortened patent term, due to the extended prosecution in the parent application.

CONCLUSION

In light of the above amendments and remarks, Applicants submit that the present application is fully in condition for allowance, and request that the Examiner withdraw the outstanding objections/rejections. Early notice to that effect is earnestly solicited.

If the Examiner contemplates other action, or if a telephone conference would expedite allowance of the claims, Applicants invite the Examiner to contact the undersigned at the number listed below.

Please charge Deposit Account No. **09-0108** in the amount of **$446.00** as set forth in the enclosed fee transmittal letter. If the USPTO determines that an additional fee is necessary, please charge any required fee to Deposit Account No. 09-0108.

Respectfully submitted,

INCYTE CORPORATION

Date: August 15, 2003

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